

# **Population Genetics of Black Bears on the Kenai Peninsula**

**Stacie Robinson \* University of Idaho**

**Lisette Waits \* University of Idaho**

**Ian Martin \* Kenai Fjords NP**

# Overview

- ❑ Objectives
- ❑ Study Area
- ❑ Project Activities
- ❑ Genetic Methodology
- ❑ Key Findings
- ❑ New Questions & Future Directions



# Objectives



- ❑ **Contribute to a science-based management plan**
- ❑ **Collect DNA samples from black bears**
- ❑ **Examine female gene flow using mtDNA**
- ❑ **Examine fine scale population structure of Kenai black bears with nuclear DNA microsatellites**
- ❑ **Evaluate environmental variables affecting black bear gene flow across the Kenai peninsula**



# National Park Participation



## Kenai Fjords National Park



# Study Area

Nuka Bay, Aialik Bay, Two Arm Bay



# Project Activities

## Field Work

Sample Collection



## Lab Work

DNA Extraction

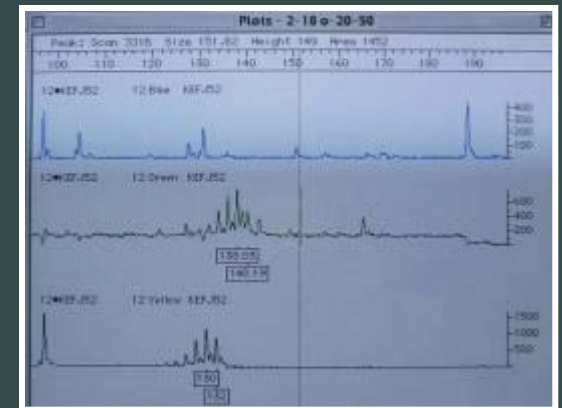
Marker Amplification

Genotyping



## Analysis

Population Structure





# Sample Collection

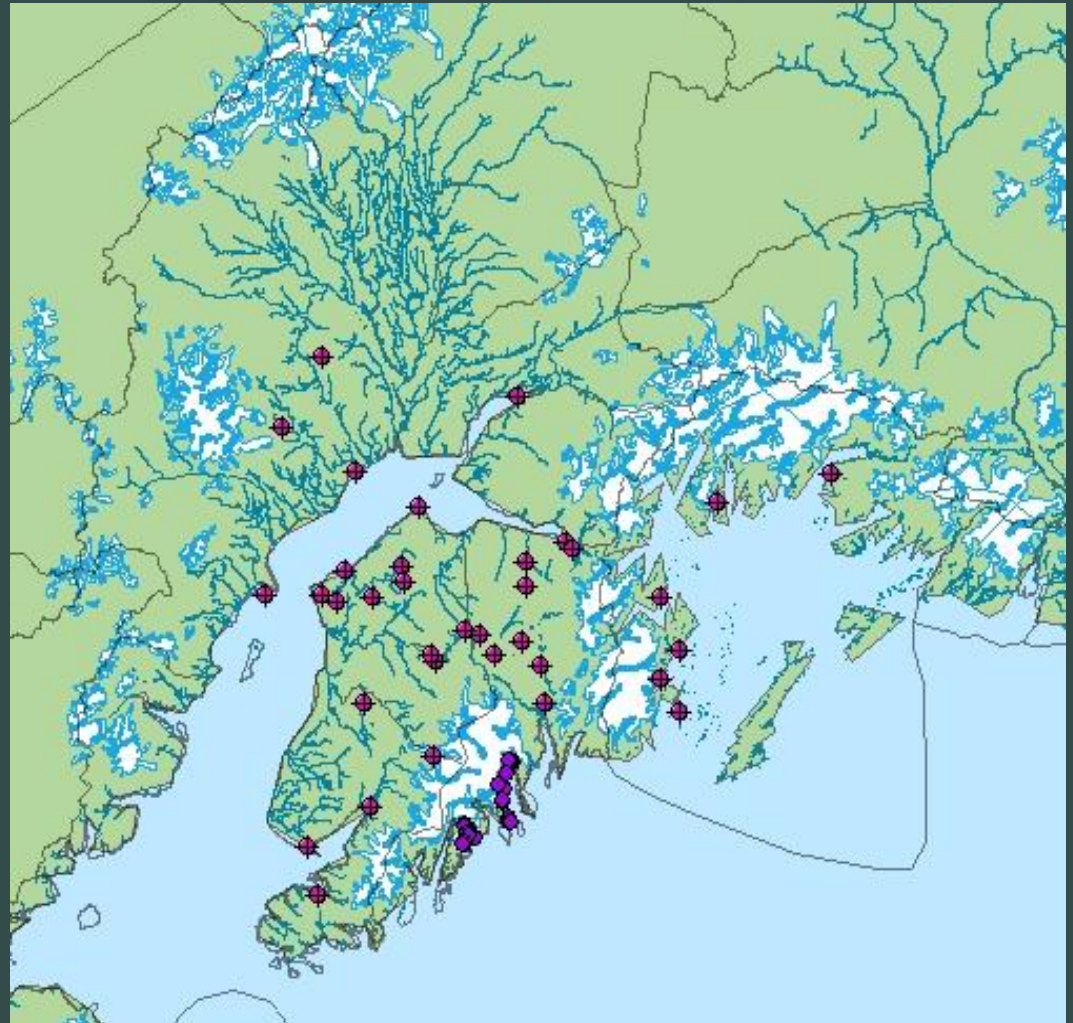
Hair samples were collected near food resources with non-invasive, non-baited hair snares and barbed wires



		Sets	Samples
2003	Nuka Bay	195	190
2004	Aialik Bay	105	210
	Two Arm Bay	113	95

# Additional Samples

- ▣ ADF&G sealed  
hunter-killed bears
- ▣ Ongoing studies at  
Washington State U.





# Genetic Methodology



## Terminology

- ❑ Loci = locations in genome
- ❑ Allele = any particular expression of a gene
- ❑ Genotype = unique combination of alleles at several loci
- ❑ Individuals are identified by genotype
- ❑ Population are identified by unique distribution of allele frequencies

# Genetic Methodology



## Genetic Markers

- ❑ Genotype 13-16 nuclear microsatellite loci
- ❑ Sequence mitochondrial DNA regions

## Analytical Tools

- ❑ Allele Frequencies
- ❑ Program Structure
- ❑  $F_{st}$

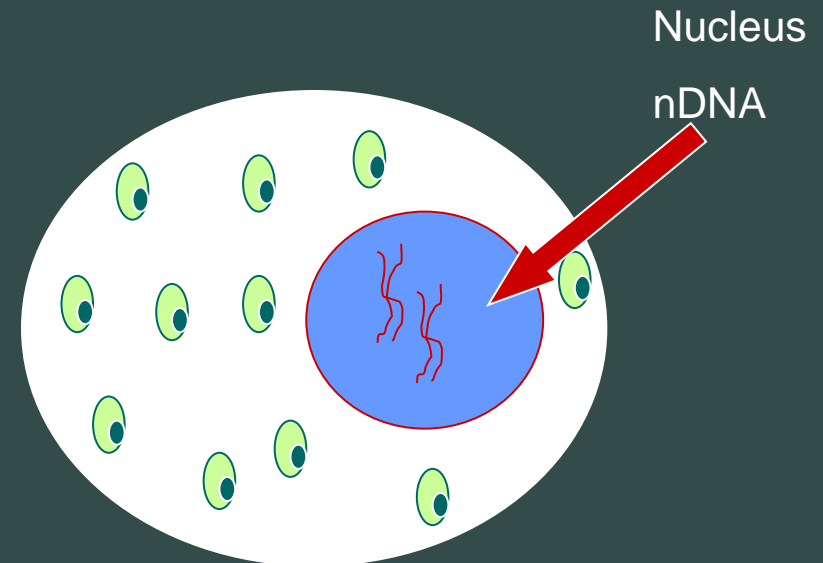
# nDNA Microsatellites

A short sequence in a variable number of repeats

GCTAATC CACACACACACACACACACACACA TACTTT

GCTAATC CACACACACACACACACAC TACTTT

- ❑ Inherited from both parents
- ❑ Rapid mutation rate
- ❑ Informative for current population trends
- ❑ Identify individuals and reveal population structure

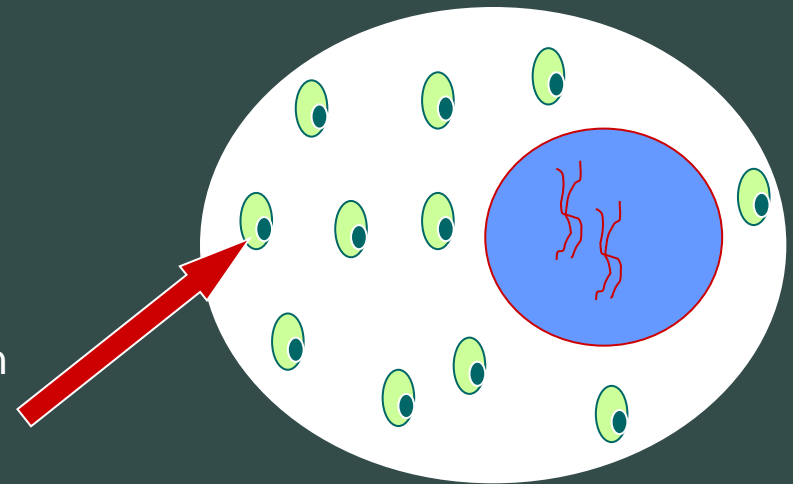




# mtDNA Sequences

- ❑ Inherited from mother to offspring
- ❑ Relatively slow mutation rates
- ❑ Informative over long time scale
- ❑ Distribution of lineages reveals flow of female genes.

Mitochondrion  
mtDNA



# Program Structure (Pritchard et al. 2000)

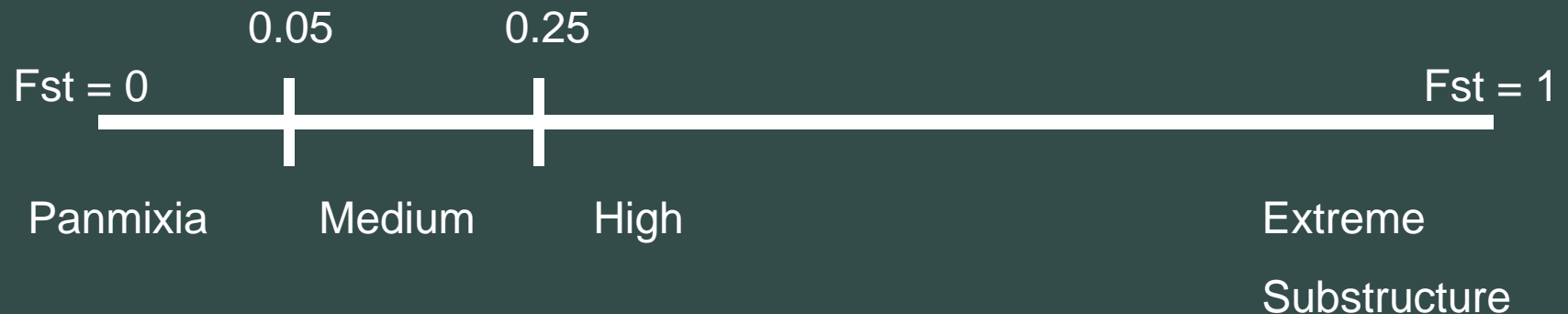
- ❑ Model-based Bayesian Approach
- ❑ Data = genotypes & allele frequencies
- ❑ Estimates the number of sub-populations  
minimizing Hardy-Weinberg and linkage disequilibrium
- ❑ Assigns individuals to each sub-population  
based upon percentage of ancestry

# Population Isolation - $F_{st}$



$F_{st}$  measures how much of the total variation is partitioned into sub-populations (Wright 1969).

Used as a measure of isolation.



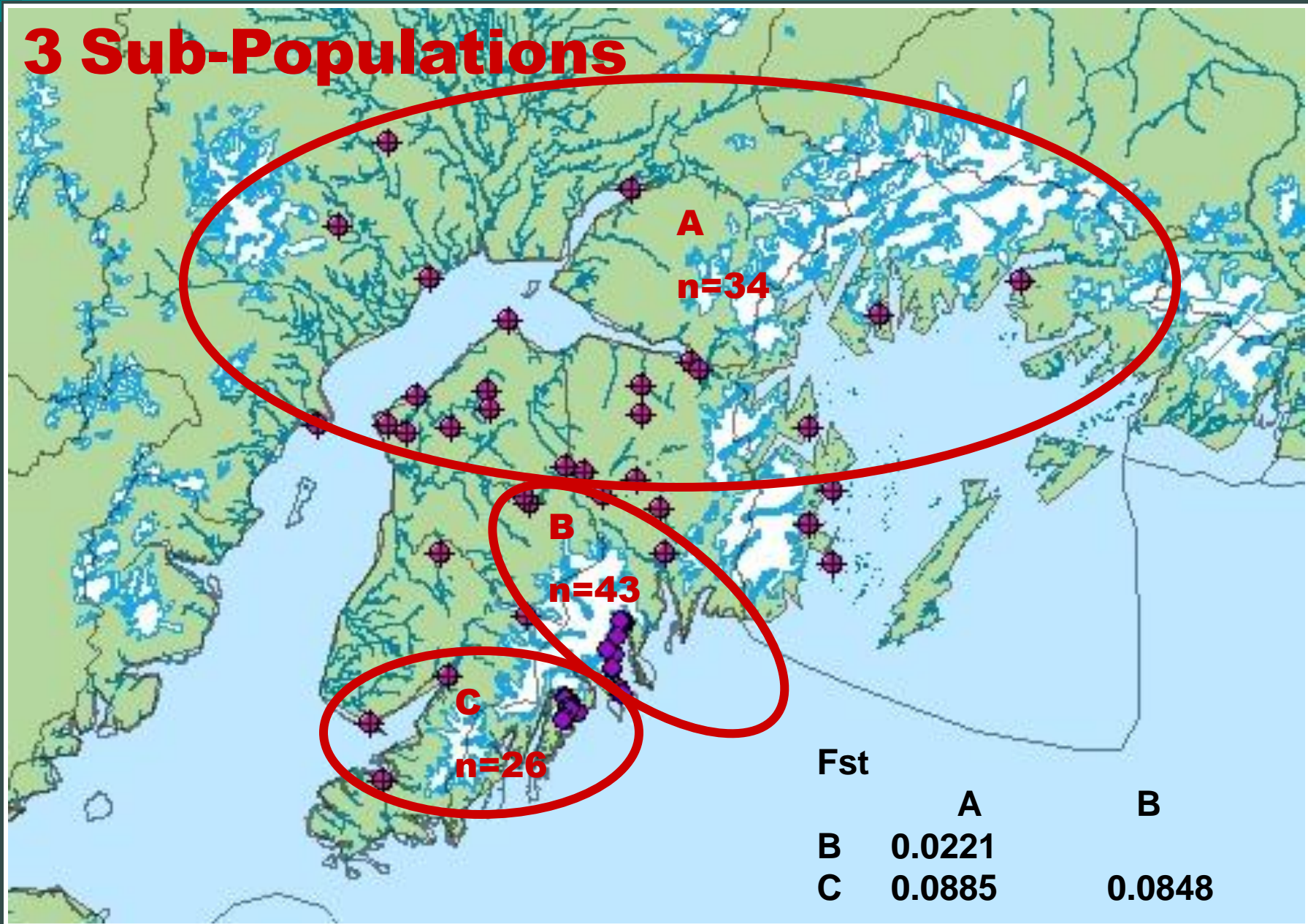


# Key Findings

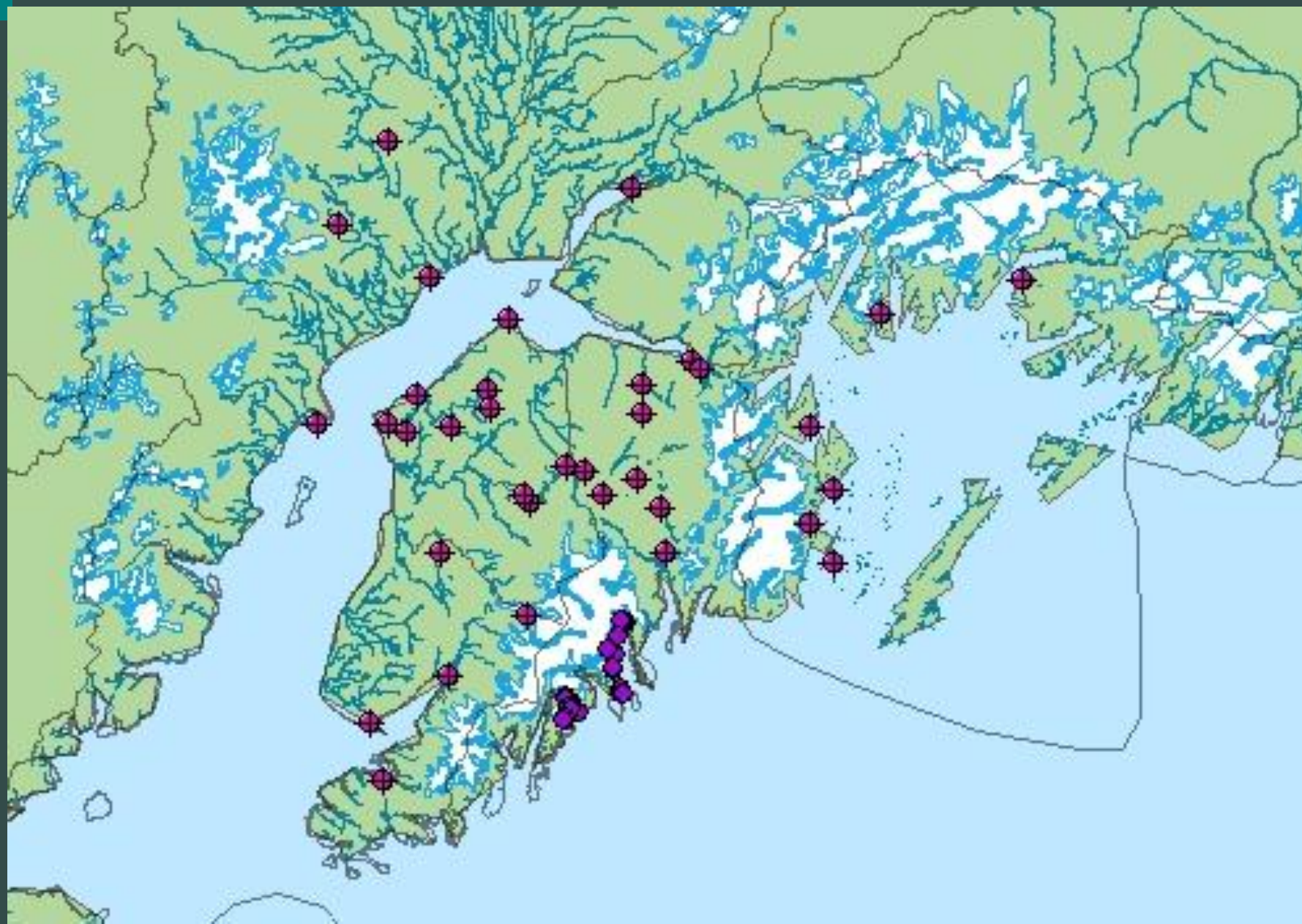


- ❑ Kenai black bears constitute a metapopulation containing 3-4 sub-populations
- ❑ Sub-populations are distinct yet connected through frequent migration
- ❑ Kenai Fjords NP contains 2 distinct sub-populations
- ❑ Matrilineal structure corroborates nDNA findings
- ❑ Unique lineages occur on the Kenai and within Kenai Fjords

# 3 Sub-Populations

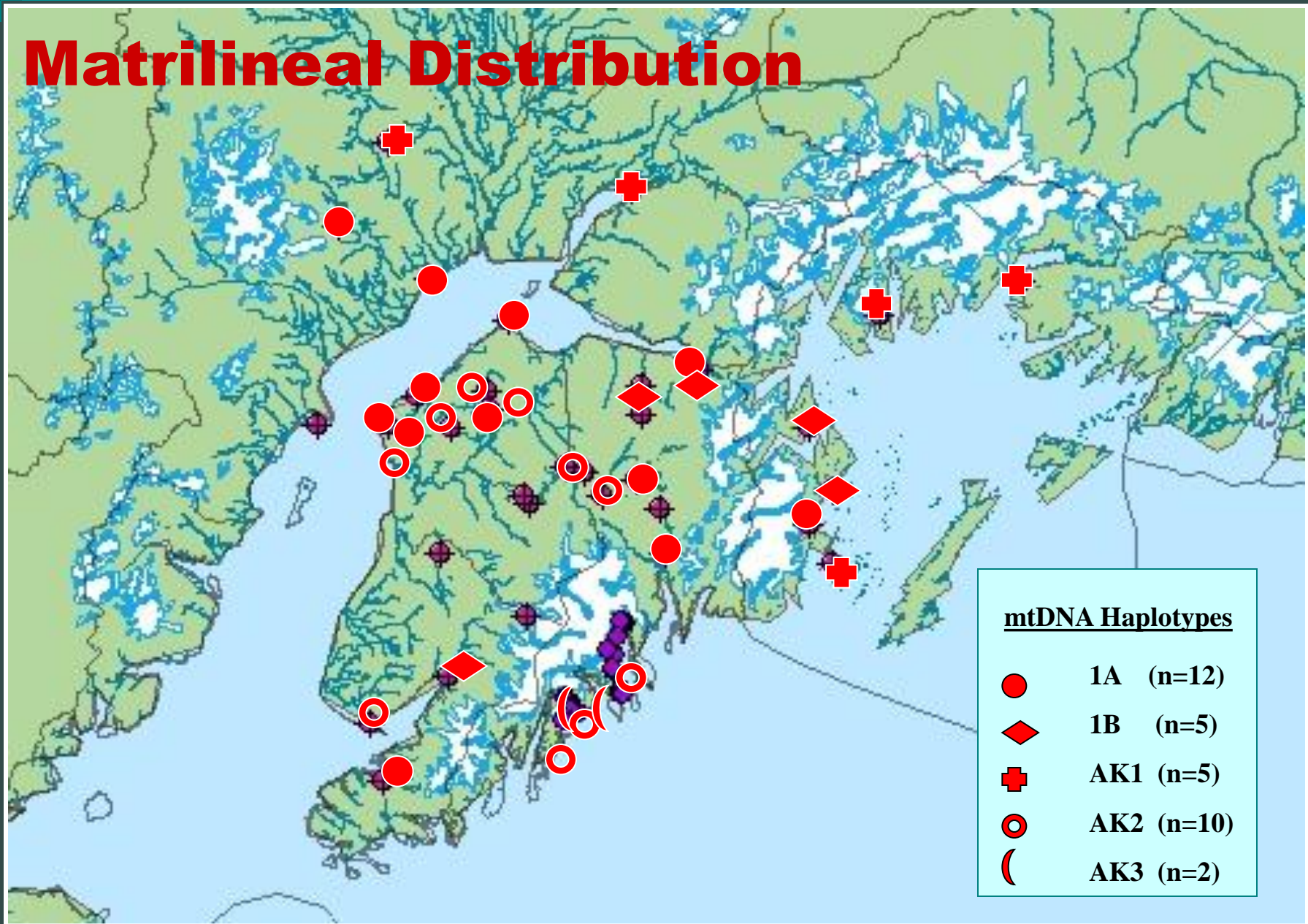








# Matrilineal Distribution



# Implications for Monitoring



- ❑ Opportunity to understand landscape ecology of black bears
- ❑ Baseline information for monitoring habitat and gene flow changes as glaciers recede with climate change
- ❑ Identify important corridors for population connectivity
- ❑ Identify source or sink sub-populations in the metapopulation
- ❑ Determine connection between park and hunted populations

# New Questions Generated



- ❑ What environmental variables influence the population structure of black bears on the Kenai?
- ❑ What barriers exist between sub-populations?
- ❑ How does Harris Bay fall between Northern and Southern Kenai Fjords sub-populations?

# Geographic Factors

- ❑ Glaciers
- ❑ Water
- ❑ Elevation





# Biological Factors

- ❑ Salmon availability
- ❑ Brown bear populations



# Future Directions



- ❑ Analyze genetic data in the landscape context using geospatial statistics, GIS
- ❑ Assess putative barriers to gene flow
- ❑ Determine environmental variable with influence on population structure and gene flow



# 2005 Field Season

- ❑ Increase sample size beyond Kenai Fjords NP

ADF&G sealed bears

Kenai NWR

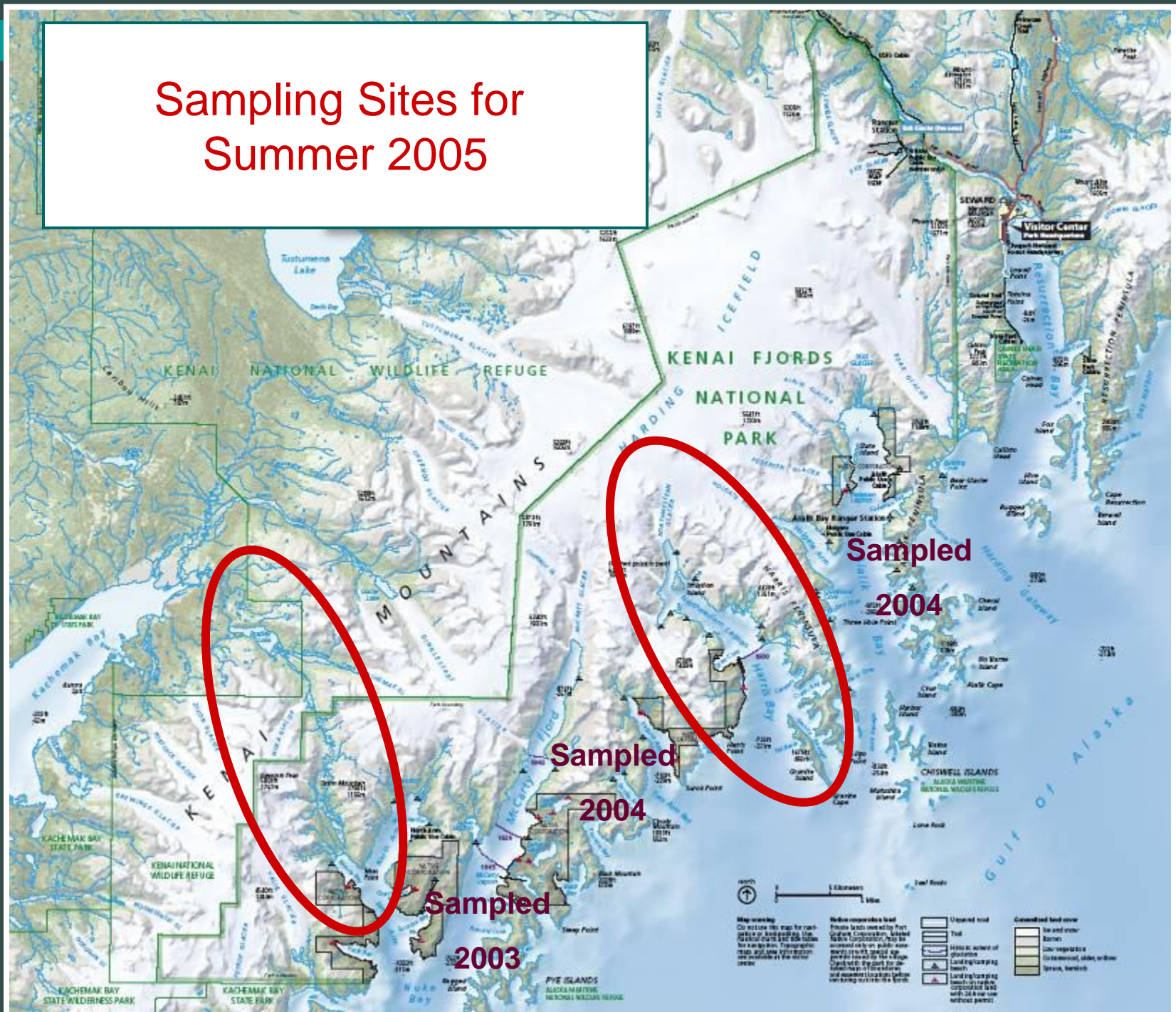
- ❑ Sample areas at sub-population breaks

Harris Bay

Nuka River



# Sampling Sites for Summer 2005



# Acknowledgements



Kenai Fjords NP

Staff & volunteers

University of Idaho LECG lab

ADF&G

Kenai NWR

Work study assistants





**Any  
Questions  
?**